Package ‘TurboNorm’

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Type Package

Title A fast scatterplot smoother suitable for microarray normalization

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Author Maarten van Iterson and Chantal van Leeuwen

Maintainer Maarten van Iterson <`mviterson@gmail.com`>

Description A fast scatterplot smoother based on B-splines with second-order difference penalty. Functions for microarray normalization of single-colour data i.e. Affymetrix/Illumina and two-colour data supplied as marray MarrayRaw-objects or limma RGList-objects are available.

License LGPL

LazyLoad yes

Depends R (>= 2.12.0), convert, limma (>= 1.7.0), marray

Imports stats, grDevices, affy, lattice

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Contents

`TurboNorm-package` *A fast scatterplot smoother with applications for microarray normalization*

Description

A fast scatterplot smoother based on B-splines with second order difference penalty. Functions for microarray normalization of single-colour data i.e. Affymetrix/Illumina and two-colour data supplied as marray MarrayRaw-objects or limma RGList-objects are available.

Details

Package:	TurboNorm
Type:	Package
Version:	1.7.2
Date:	2013-29-01
License:	LGPL
LazyLoad:	yes

This package contains an implementation of piecewise constant P-splines of Eilers and Marx (1996) that can be used for normalization of either single- or two-colour data. For two-colour data objects of type `RGList` from the `limma` package and `MarrayRaw` from the package `marray` can be normalized using the function `pspline()`. For single colour microarray data wrapper functions are written based on the `affy` package functions `normalize.loess()` and `normalize.AffyBatch.loess()` namely `normalize.pspline()` and `normalize.AffyBatch.pspline()`. Also a `panel.pspline()` is available for adding the smoothed curve to `lattice` graphics panels.

Note

The package pspline (S original by Jim Ramsey, R port by Brian Ripley) implements the B-spline/Natural Cubic Spline smoother

Author(s)

Chantal van Leeuwen and Maarten van Iterson Maintainer: Maarten van Iterson<mviterson@gmail.com>

References

van Iterson M, Duijkers FA, Meijerink JP, Admiraal P, van Ommen GJ, Boer JM, van Noesel MM, Menezes RX (2012). A novel and fast normalization method for high-density arrays. SAGMB, 11(4).

Paul .H.C. Eilers and Brain D. Marx (1996). Flexible smoothing with B-splines and Penalties. Statistical Science, Vol 11, No. 2, 89-121.

See Also

`turbotrend`, `pspline`, `normalize.pspline`, `normalize.AffyBatch.pspline`, `panel.pspline`

`methylation` *CpG island DNA methylation array data*

Description

CpG island DNA methylation array data of a neuro-ectodermal cell line that was treated with a demethylating agent

Usage

```
data(methylation)
```

Format

"RGList" as defined in the package limma containing data from CpG island DNA methylation array data of a neuro-ectodermal cell line that was treated with a demethylating agent. The element "weights" of the "RGList" contains the subset of invariant fragments, those without methylation-sensitive restriction sites, as a logical vector.

Details

The data is extracted from a larger experiment described in van Iterson et al. Because the data is from a high-dense tiling array a random subset of the data was chosen for convenience in making the vignette.

References

van Iterson M, Duijkers FA, Meijerink JP, Admiraal P, van Ommen GJ, Boer JM, van Noesel MM, Menezes RX (2012). A novel and fast normalization method for high-density arrays. SAGMB, 11(4).

Examples

```
data(methylation)
```

`normalize.pspline` *Functions for single-colour microarray data normalization using the P-splines*

Description

Modified version of normalize.loess and normalize.AffyBatch.pspline from the affy package uses the P-spline smoother in stead of the loess algorithm

Usage

```
normalize.pspline(mat, epsilon = 10^-2, maxit = 1, log.it = TRUE,
    verbose = TRUE, weights = rep(1, nrow(mat)), ...)
normalize.AffyBatch.pspline(abatch,
    type=c("together","pmonly","mmonly","separate"), ...)
```

Arguments

`mat`	a matrix with columns containing the values of the chips to normalize.
`abatch`	an `AffyBatch` object.
`epsilon`	a tolerance value (supposed to be a small value - used as a stopping criterion).
`maxit`	maximum number of iterations.
`log.it`	logical. If `TRUE` it takes the log2 of `mat`
`verbose`	logical. If `TRUE` displays current pair of chip being worked on.
`weights`	For weighted normalization. The default is NULL, so there are no weights used.
`type`	A string specifying how the normalization should be applied. See details for more.
`...`	Graphical parameters can be supplied.

Details

This function is a modified version of the function `normalize.loess` from the affy package. In stead of the loess algorithm the function uses the P-spline algorithm. The type argument should be one of `"separate","pmonly","mmonly","together"` which indicates whether to normalize only one probe type(PM,MM) or both together or separately.

Value

Normalized `AffyBatch`

Author(s)

Maarten van Iterson and Chantal van Leeuwen

References

Laurent Gautier, Leslie Cope, Benjamin M. Bolstad and Rafael A. Irizarry (2004). affy -analysis of Affymetrix GeneChip data at the probe level. Bioinformatics, Vol. 20, no. 3, 307-315.

van Iterson M, Duijkers FA, Meijerink JP, Admiraal P, van Ommen GJ, Boer JM, van Noesel MM, Menezes RX (2012). A novel and fast normalization method for high-density arrays. SAGMB, 11(4).

Paul .H.C. Eilers and Brain D. Marx (1996). Flexible smoothing with B-splines and Penalties. Statistical Science, Vol 11, No. 2, 89-121.

See Also

`normalize.loess`

Examples

```
library(affydata)
data(Dilution)
PM <- log2(pm(Dilution[,c(1,3)]))
M <- PM[,1]-PM[,2]
A <- 0.5*(PM[,1]+PM[,2])

nPM <- log2(normalize.pspline(pm(Dilution[,c(1,3)])))
nM <- nPM[,1]-nPM[,2]
nA <- 0.5*(nPM[,1]+nPM[,2])

par(mfcol=c(2,1))
plot(M~A)
plot(nM~nA)

norm <- normalize.AffyBatch.pspline(Dilution, type="pmonly")

weights <- rep(1, nrow(exprs(Dilution)))
normw <- normalize.AffyBatch.pspline(Dilution, type="pmonly", weights=weights)
```

`panel.pspline` *Panel function for adding a P-spline smoothed curves to a lattice graphics panel*

Description

The function panel.pspline is similar to panel.loess but show the P-spline smoothed curve.

Usage

```
panel.pspline(x, y, weights = rep(1, length(y)), nintervals = 100, type, horizontal = FALSE, col.line=1
```

Arguments

`x, y`	vectors giving the coordinates of the points in the scatter plot
`weights`	vector of weights of with same length as the data for a weighted smoothing. Default all weights are 1.
`nintervals`	an integer indicating the number of intervals equal to 1 + number of knots. Currently the intervals must be langer than 10.
`type`	see `panel.loess`
`horizontal`	see `panel.loess`
`col.line, lty, lwd`	line colour, type and width that will be used in the plots, defaults are col=1, lty=1 and lwd=1.
`...`	see `panel.loess`

Details

?panel.loess

Author(s)

Maarten van Iterson and Chantal van Leeuwen

References

Deepayan Sarkar (2009). lattice: Lattice Graphics. R package version 0.17-26. http://CRAN.R-project.org/package=lattice

van Iterson M, Duijkers FA, Meijerink JP, Admiraal P, van Ommen GJ, Boer JM, van Noesel MM, Menezes RX (2012). A novel and fast normalization method for high-density arrays. SAGMB, 11(4).

Paul .H.C. Eilers and Brain D. Marx (1996). Flexible smoothing with B-splines and Penalties. Statistical Science, Vol 11, No. 2, 89-121.

See Also

`panel.loess`

Examples

```
library(marray)
library(lattice)
data(swirl)
data <- data.frame(M=as.vector(maM(swirl)), A=as.vector(maA(swirl)), Sample=rep(paste("Array", 1:4), each=nrow(s

xyplot(M~A|Sample, data=data,
                        panel = function(x, y) {
            panel.grid(h=-1, v= 2)
            panel.xyplot(x, y)
            panel.loess(x, y, span=0.25, col="black")
                                                panel.pspline(x, y, col="red", lwd=2)})
```

`pspline` *Function for two-colour microarray data normalization using the P-splines*

Description

Wrapper function for two colour microarray data normalization using the P-spline smoother suitable for a RGList- or MarrayRaw-objects.

Usage

```
pspline(object, background = c("none", "substract"), weights = NULL, nintervals = 100, subset=NULL, sho
```

Arguments

`object`	either a RGList or an MarrayRaw-object.
`background`	for background substraction use 'substract'. Default is no backgroud substraction.
`weights`	vector of weights that will be used a for a weighted normalization. The default `NULL` assumse equal weight `1` for all data points.
`nintervals`	number of bins in which the data will be divided. The default is 100 bins.
`showArrays`	either a integer(> 0) or a vector of integers indicating the arrays for which a MA-plot will be produced.
`subset`	subset of the data on which the normalization will be based. A special case of weighted normalization.
`verbose`	if `TRUE` gives additional information on the fit
.	
`line.col`, `line.lty`, `line.lwd`	line colour, type and width that will be used in the plots, defaults are col=2, lty=1 and lwd=2.
`...`	additional graphical arguments for plotting.

Details

if necessary?

Value

The value that will be returned is either a MAList or MarrayNorm-object dependening on the input type.

Author(s)

Chantal van Leeuwen and Maarten van Iterson

References

van Iterson M, Duijkers FA, Meijerink JP, Admiraal P, van Ommen GJ, Boer JM, van Noesel MM, Menezes RX (2012). A novel and fast normalization method for high-density arrays. SAGMB, 11(4).

Paul .H.C. Eilers and Brain D. Marx (1996). Flexible smoothing with B-splines and Penalties. Statistical Science, Vol 11, No. 2, 89-121.

See Also

`normalizeWithinArrays`, `maNormMain`

Examples

```
library(marray)
data(swirl)

x <- pspline(swirl, showArrays=2, pch=20, col="grey")
x <- pspline(swirl, showArrays=2:4, line.col="green")
```

`turbotrend` *turbotrend: a fast scatterplot smoother*

Description

A fast scatterplot smoother based on B-splines with second order difference penalty

Usage

```
turbotrend(x, y, w = rep(1, length(y)), n = 100, lambda=10^seq(-10, 10, length=1000), iter=0, method=c('
```

Arguments

`x, y`	vectors giving the coordinates of the points in the scatter plot.
`w`	vector of weights of with same length as the data for a weighted smoothing. Default all weights are 1.
`n`	an integer indicating the number of intervals equal to 1 + number of knots. Currently the intervals must be langer than 10.
`lambda`	Optionally a user-defined penalty parameter can be provided, if not generalized cross-validation is used to find the optimal penalty parameter.
`iter`	Number of robustifying iterations similar as lowess.
`method`	method for solving the system of linear equations either using the data in the original space or transformed to the Demmler-Reinsch basis.

Details

some details about implementation

Value

An object of type `pspline` is returned as a list with the following items:

`x`	original data vector x
`y`	fitted y-values with same length as vector x
`w`	vector of weights
`n`	number of bins
`ytrend`	binnend fitted y-values
`xtrend`	binned x-values
`lambda`	if scalar penalty parameter used else if vector of two lower and upper bound of the grid
`iter`	number of robustifying iterations
`gcv`	generalized cross-validation
`edf`	effective degrees of freedom (trace of the smoother matrix)
`call`	function call which produced this output

Author(s)

Maarten van Iterson, Chantal van Leeuwen

References

van Iterson M, Duijkers FA, Meijerink JP, Admiraal P, van Ommen GJ, Boer JM, van Noesel MM, Menezes RX (2012). A novel and fast normalization method for high-density arrays. SAGMB, 11(4).

Paul .H.C. Eilers and Brain D. Marx (1996). Flexible smoothing with B-splines and Penalties. Statistical Science, Vol 11, No. 2, 89-121.

See Also

`loess`,`lowess`, `smooth`, `smooth.spline` and `smooth.Pspline`

Examples

```
library(marray)
data(swirl)

x <- maA(swirl)[,1]
y <- maM(swirl)[,1]
xord <- x[order(x)]
yord <- y[order(x)]

plot(xord, yord, main = "data(swirl)  &  smoothing splines + lowess")
lines(turbotrend(xord, yord), col = "red", lwd=2)
lines(smooth.spline(xord, yord), col = "green", lwd=2)
lines(lowess(xord, yord), col = "purple", lwd=2)
legend("topleft", c("piecewise constant P-splines", "Cubic B-splines", "lowess"), text.col=c("red","green","purpl
```

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